

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Alderson, Mark R.
Goodwin, Raymond G.
Smith, Craig A.

(ii) TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand And Human Receptor That Binds Thereto

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Kathryn A. Seese, Immunex Corporation
(B) STREET: 51 University Street
(C) CITY: Seattle
(D) STATE: Washington
(E) COUNTRY: US
(F) ZIP: 98101

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Seese, Kathryn A.
(B) REGISTRATION NUMBER: 32,172
(C) REFERENCE/DOCKET NUMBER: 2801-WO

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (206) 587-0430
(B) TELEFAX: (206) 233-0644

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: murine 4-1BB-L

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 53..979

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: *luc*, L

AGCCTATAAA	GCACGGGCAC	TGGCGGGAGA	CGTGCAGTGA	CCGACCGTGG	TA	ATG	55
						Met	
						1	
GAC	CAG	CAC	ACA	CTT	GAT	GTG	103
Asp	Gln	His	Thr	Leu	Asp	Val	
5	10	15					
GCA	GGT	ACT	TCG	TGC	CCC	TCG	51
Ala	Gly	Thr	Ser	Cys	Pro	Ser	
20	25	30					
CTC	CTC	GCG	GAC	GCT	GCG	CTC	199
Leu	Leu	Ala	Asp	Ala	Ala	Leu	
35	40	45					
GCC	GCG	CTC	CCC	ACG	GAT	GCT	247
Ala	Ala	Leu	Pro	Thr	Asp	Ala	
50	55	60					
CGC	GAG	GCC	GCG	TGG	CCG	CCT	295
Arg	Glu	Ala	Ala	Trp	Pro	Pro	
70	75	80					
AAG	CTC	TAT	GGC	CTA	GTC	GCT	343
Lys	Leu	Tyr	Gly	Leu	Val	Ala	
85	90	95					
TGT	GTT	CCT	ATC	TTC	ACC	CGC	391
Cys	Val	Pro	Ile	Phe	Thr	Arg	
100	105	110					
ACC	ACC	TCG	CCC	AAC	CTG	GGT	439
Thr	Thr	Ser	Pro	Asn	Leu	Gly	
115	120	125					
ACC	CCT	GTT	TCC	CAC	ATT	GGC	487
Thr	Pro	Val	Ser	His	Ile	Gly	
130	135	140					
CCT	GTG	TTC	GCC	AAG	CTA	CTG	535
Pro	Val	Phe	Ala	Lys	Leu	Ala	
150	155	160					
ACA	ACT	CTG	AAC	TGG	CAC	AGC	583
Thr	Thr	Leu	Asn	Trp	His	Ser	
165	170	175					
TCT	CAA	GGT	CTG	AGG	TAC	GAA	631
Ser	Gln	Gly	Leu	Arg	Tyr	Glu	
180	185	190					

AGT CCC GGG CTC TAC TAC GTA TTT TTG GAA CTG AAG CTC AGT CCA ACA Ser Pro Gly Leu Tyr Tyr Val Phe Leu Glu Leu Lys Leu Ser Pro Thr 195 200 205	679
TTC ACA AAC ACA GGC CAC AAG GTG CAG GGC TGG GTC TCT CTT GTT TTG Phe Thr Asn Thr Gly His Lys Val Gln Gly Trp Val Ser Leu Val Leu 210 215 220 225	727
CAA GCA AAG CCT CAG GTA GAT GAC TTT GAC AAC TTG GCC CTG ACA GTG Gln Ala Lys Pro Gln Val Asp Asp Phe Asp Asn Leu Ala Leu Thr Val 230 235 240	775
GAA CTG TTC CCT TGC TCC ATG GAG AAC AAG TTA GTG GAC CGT TCC TGG Glu Leu Phe Pro Cys Ser Met Glu Asn Lys Leu Val Asp Arg Ser Trp 245 250 255	823
AGT CAA CTG TTG CTC CTG AAG GCT GGC CAC CGC CTC AGT GTG GGT CTG Ser Gln Leu Leu Leu Lys Ala Gly His Arg Leu Ser Val Gly Leu 260 265 270	871
AGG GCT TAT CTG CAT GGA GCC CAG GAT GCA TAC AGA GAC TGG GAG CTG Arg Ala Tyr Leu His Gly Ala Gln Asp Ala Tyr Arg Asp Trp Glu Leu 275 280 285	919
TCT TAT CCC AAC ACC ACC AGC TTT GGA CTC TTT CTT GTG AAA CCC GAC Ser Tyr Pro Asn Thr Ser Phe Gly Leu Phe Leu Val Lys Pro Asp 290 295 300 305	967
AAC CCA TGG GAA TGAGAACTAT CCTCTTGTG ACTCCTAGTT GCTAAGTCCT Asn Pro Trp Glu	1019
CAAAGCTGCTA TGTTTATGG GGTCTGAGCA GGGGTCCCTT CCATGACTTT CTCTTGTCTT	1079
TAACCTGGACT TGGTATTAT TCTGAGCATA GCTCAGACAA GACTTTATAT AATTCACTAG	1139
ATAGCATTAG TAAACTGCTG GGCAGCTGCT AGATAAAAAAA AAATTTCTAA ATCAAAGTTT	1199
ATATTTATAT TAATATATAA AAATAAATGT GTTTGTAAAT AAAAAAAA AAAAA	1254

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: Met Asp Gln His Thr Leu Asp Val Glu Asp Thr Ala Asp Ala Arg His

Met Asp Gln His Thr Leu Asp Val Glu Asp Thr Ala Asp Ala Arg His 1 5 10 15
Pro Ala Gly Thr Ser Cys Pro Ser Asp Ala Ala Leu Leu Arg Asp Thr 20 25 30
Gly Leu Leu Ala Asp Ala Ala Leu Leu Ser Asp Thr Val Arg Pro Thr 35 40 45

Asn	Ala	Ala	Leu	Pro	Thr	Asp	Ala	Ala	Tyr	Pro	Ala	Val	Asn	Val	Arg
50						55				60					
Asp	Arg	Glu	Ala	Ala	Trp	Pro	Pro	Ala	Leu	Asn	Phe	Cys	Ser	Arg	His
65					70				75					80	
Pro	Lys	Leu	Tyr	Gly	Leu	Val	Ala	Leu	Val	Leu	Leu	Leu	Ile	Ala	
						85				90				95	
Ala	Cys	Val	Pro	Ile	Phe	Thr	Arg	Thr	Glu	Pro	Arg	Pro	Ala	Leu	Thr
						100			105				110		
Ile	Thr	Thr	Ser	Pro	Asn	Leu	Gly	Thr	Arg	Glu	Asn	Asn	Ala	Asp	Gln
						115			120				125		
Val	Thr	Pro	Val	Ser	His	Ile	Gly	Cys	Pro	Asn	Thr	Thr	Gln	Gln	Gly
						130			135			140			
Ser	Pro	Val	Phe	Ala	Lys	Leu	Leu	Ala	Lys	Asn	Gln	Ala	Ser	Leu	Cys
						145			150			155		—	160
Asn	Thr	Thr	Leu	Asn	Trp	His	Ser	Gln	Asp	Gly	Ala	Gly	Ser	Ser	Tyr
						165			170				175		
Leu	Ser	Gln	Gly	Leu	Arg	Tyr	Glu	Glu	Asp	Lys	Lys	Glu	Leu	Val	Val
						180			185				190		
Asp	Ser	Pro	Gly	Leu	Tyr	Tyr	Val	Phe	Leu	Glu	Leu	Lys	Leu	Ser	Pro
						195			200			205			
Thr	Phe	Thr	Asn	Thr	Gly	His	Lys	Val	Gln	Gly	Trp	Val	Ser	Leu	Val
						210			215			220			
Leu	Gln	Ala	Lys	Pro	Gln	Val	Asp	Asp	Phe	Asp	Asn	Leu	Ala	Leu	Thr
						225			230			235			240
Val	Glu	Leu	Phe	Pro	Cys	Ser	Met	Glu	Asn	Lys	Leu	Val	Asp	Arg	Ser
						245			250				255		
Trp	Ser	Gln	Leu	Leu	Leu	Lys	Ala	Gly	His	Arg	Leu	Ser	Val	Gly	
						260			265			270			
Leu	Arg	Ala	Tyr	Leu	His	Gly	Ala	Gln	Asp	Ala	Tyr	Arg	Asp	Trp	Glu
						275			280			285			
Leu	Ser	Tyr	Pro	Asn	Thr	Thr	Ser	Phe	Gly	Leu	Phe	Leu	Val	Lys	Pro
						290			295			300			
Asp	Asn	Pro	Trp	Glu											
					305										

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1619 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: human 4-1BB-L(7A)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 4..765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: human, L

GTC ATG GAA TAC GCC TCT GAC GCT TCA CTG GAC CCC GAA GCC CCG TGG	48
Met Glu Tyr Ala Ser Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp	
1 5 10 15	
—	
CCT CCC GCG CCC CGC GCT CGC GCC TGC CGC GTA CTG CCT TGG GCC CTG	96
Pro Pro Ala Pro Arg Ala Arg Ala Cys Arg Val Leu Pro Trp Ala Leu	
20 25 30	
—	
GTC GCG GGG CTG CTG CTG CTG CTC GCT GCC GCC TGC GCC GTC	144
Val Ala Gly Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val	
35 40 45	
—	
TTC CTC GCC TGC CCC TGG GCC GTG TCC GGG GCT CGC GCC TCG CCC GGC	192
Phe Leu Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly	
50 55 60	
—	
TCC GCG GCC AGC CCG AGA CTC CGC GAG GGT CCC GAG CTT TCG CCC GAC	240
Ser Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp	
65 70 75	
—	
GAT CCC GCC GGC CTC TTG GAC CTG CGG CAG GGC ATG TTT GCG CAG CTG	288
Asp Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu	
80 85 90 95	
—	
GTG GCC CAA AAT GTT CTG CTG ATC GAT GGG CCC CTG AGC TGG TAC AGT	336
Val Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser	
100 105 110	
—	
GAC CCA GGC CTG GCA GGC GTG TCC CTG ACG GGG GGC CTG AGC TAC AAA	384
Asp Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys	
115 120 125	
—	
GAG GAC ACG AAG GAG CTG GTG GCC AAG GCT GGA GTC TAC TAT GTC	432
Glu Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val	
130 135 140	
—	
TTC TTT CAA CTA GAG CTG CGG CGC GTG GTG GCC GGC GAG GGC TCA GGC	480
Phe Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly	
145 150 155	
—	
TCC GTT TCA CTT GCG CTG CAC CTG CAG CCA CTG CGC TCT GCT GCT GGG	528
Ser Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly	
160 165 170 175	

GCC	GCC	GCC	CTG	GCT	TTG	ACC	GTG	GAC	CTG	CCA	CCC	GCC	TCC	TCC	GAG	576
Ala	Ala	Ala	Leu	Ala	Leu	Thr	Val	Asp	Leu	Pro	Pro	Ala	Ser	Ser	Glu	
180									185						190	
GCT	CGG	AAC	TCG	GCC	TTC	GGT	TTC	CAG	GGC	CGC	TTG	CTG	CAC	CTG	AGT	624
Ala	Arg	Asn	Ser	Ala	Phe	Gly	Phe	Gln	Gly	Arg	Leu	Leu	His	Leu	Ser	
195								200						205		
GCC	GGC	CAG	CGC	CTG	GGC	GTC	CAT	CTT	CAC	ACT	GAG	GCC	AGG	GCA	CGC	672
Ala	Gly	Gln	Arg	Leu	Gly	Val	His	Leu	His	Thr	Glu	Ala	Arg	Ala	Arg	
									215						220	
210																
CAT	GCC	TGG	CAG	CTT	ACC	CAG	GGC	GCC	ACA	GTC	TTG	GGA	CTC	TTC	CGG	720
His	Ala	Trp	Gln	Leu	Thr	Gln	Gly	Ala	Thr	Val	Leu	Gly	Leu	Phe	Arg	
									230						235	
225																
GTG	ACC	CCC	GAA	ATC	CCA	GCC	GGA	CTC	CCT	TCA	CCG	AGG	TCG	GAA		765
Val	Thr	Pro	Glu	Ile	Pro	Ala	Gly	Leu	Pro	Ser	Pro	Arg	Ser	Glu		
									245						250	
240																
AACGCCAGC	CTGGGTGCAG	CCCACCTGGA	CAGAGTCCGA	ATCCTACTCC	ATCCTTCATG											826
GAGACCCCTG	GTGCTGGTC	CCTGCTGCTT	TCTCTACCTC	AAGGGGCTTG	GCAGGGGTCC											886
CTGCTGCTGA	CCTCCCTTG	AGGACCCCTCC	TCACCCACTC	CTTCCCCAAG	TTGGACCTTG											946
ATATTTATTC	TGAGCCTGAG	CTCAGATAAT	ATATTATATA	TATTATATAT	ATATATATAT											1006
TTCTATTTAA	AGAGGATCCT	GAGTTGTGA	ATGGACTTTT	TTAGAGGAGT	TGTTTGCGGG											1066
GGGGGGTCTT	CGACATTGCC	GAGGCTGGTC	TTGAACTCCT	GGACTTAGAC	GATCCTCCTG											1126
CCTCAGCCTC	CCAAGCAACT	GGGATTCATC	CTTCTATTAA	ATTCAATTGTA	CTTATTTGCC											1186
TATTTGTGTG	TATTGAGCAT	CTGTAATGTG	CCAGCATTGT	GCCCAGGCTA	GGGGGCTATA											1246
GAAACATCTA	GAAATAGACT	GAAAGAAAAT	CTGAGTTATG	GTAATACGTG	AGGAATTAA											1306
AGACTCATCC	CCAGCCTCCA	CCTCCTGTGT	GATACTTGGG	GGCTAGCTT	TTTCTTTCTT											1366
TCTTTTTTT	GAGATGGTCT	TGTTCTGTCA	ACCAGGCTAG	AATGCAGCGG	TGCAATCATG											1426
AGTCAATGCA	GCCTCCAGCC	TCGACCTCCC	GAGGCTCAGG	TGATCCTCCC	ATCTCAGCCT											1486
CTCGAGTAGC	TGGGACCACA	GTTGTGTGCC	ACCACACTTG	GCTAACCTTT	TAATTTTTTT											1546
GC GG GAGACGG	TATTGCTATG	TTGCCAAGGT	TGTTTACATG	CCAGTACAAT	TTATAATAAAA											1606
CACTCATTTC	TCC															1619

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4: *human L*

Met Glu Tyr Ala Ser Asp Ala Ser Leu Asp Pro Glu Ala Pro Trp Pro
1 5 10 15

Pro Ala Pro Arg Ala Arg Ala Cys Arg Val Leu Pro Trp Ala Leu Val
20 25 30

Ala Gly Leu Leu Leu Leu Leu Leu Ala Ala Ala Cys Ala Val Phe
35 40 45

Leu Ala Cys Pro Trp Ala Val Ser Gly Ala Arg Ala Ser Pro Gly Ser
50 55 60

Ala Ala Ser Pro Arg Leu Arg Glu Gly Pro Glu Leu Ser Pro Asp Asp
65 70 75 80

Pro Ala Gly Leu Leu Asp Leu Arg Gln Gly Met Phe Ala Gln Leu Val
85 90 95

Ala Gln Asn Val Leu Leu Ile Asp Gly Pro Leu Ser Trp Tyr Ser Asp
100 105 110

Pro Gly Leu Ala Gly Val Ser Leu Thr Gly Gly Leu Ser Tyr Lys Glu
115 120 125

Asp Thr Lys Glu Leu Val Val Ala Lys Ala Gly Val Tyr Tyr Val Phe
130 135 140

Phe Gln Leu Glu Leu Arg Arg Val Val Ala Gly Glu Gly Ser Gly Ser
145 150 155 160

Val Ser Leu Ala Leu His Leu Gln Pro Leu Arg Ser Ala Ala Gly Ala
165 170 175

Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu Ala
180 185 190

Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser Ala
195 200 205

Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg His
210 215 220

Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg Val
225 230 235 240

Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu
245 250

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: mu4-1BB

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..768

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 70..768

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 1..69

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG	GGA	AAC	AAC	TGT	TAC	AAC	GTG	GTG	GTC	ATT	GTG	CTG	CTG	CTG	CTA	GTG	48
Met	Gly	Asn	Asn	Cys	Tyr	Asn	Val	Val	Val	Ile	Val	Leu	Leu	Leu	Val		
-23				-20					-15						-10		
GGC	TGT	GAG	AAG	GTG	GGA	GCC	GTG	CAG	AAC	TCC	TGT	GAT	AAC	TGT	CAG	96	
Gly	Cys	Glu	Lys	Val	Gly	Ala	Val	Gln	Asn	Ser	Cys	Asp	Asn	Cys	Gln		
-5							1							5			
CCT	GGT	ACT	TTC	TGC	AGA	AAA	TAC	AAT	CCA	GTC	TGC	AAG	AGC	TGC	CCT	144	
Pro	Gly	Thr	Phe	Cys	Arg	Lys	Tyr	Asn	Pro	Val	Cys	Lys	Ser	Cys	Pro		
10					15					20					25		
CCA	AGT	ACC	TTC	TCC	AGC	ATA	GGT	GGA	CAG	CCG	AAC	TGT	AAC	ATC	TGC	192	
Pro	Ser	Thr	Phe	Ser	Ser	Ile	Gly	Gly	Gln	Pro	Asn	Cys	Asn	Ile	Cys		
					30				35					40			
AGA	GTG	TGT	GCA	GGC	TAT	TTC	AGG	TTC	AAG	AAG	TTT	TGC	TCC	TCT	ACC	240	
Arg	Val	Cys	Ala	Gly	Tyr	Phe	Arg	Phe	Lys	Lys	Phe	Cys	Ser	Ser	Thr		
					45				50					55			
CAC	AAC	GCG	GAG	TGT	GAG	TGC	ATT	GAA	GGA	TTC	CAT	TGC	TTG	GGG	CCA	288	
His	Asn	Ala	Glu	Cys	Glu	Cys	Ile	Glu	Gly	Phe	His	Cys	Leu	Gly	Pro		
					60				65					70			
CAG	TGC	ACC	AGA	TGT	GAA	AAG	GAC	TGC	AGG	CCT	GGC	CAG	GAG	CTA	ACG	336	
Gln	Cys	Thr	Arg	Cys	Glu	Lys	Asp	Cys	Arg	Pro	Gly	Gln	Glu	Leu	Thr		
					75				80					85			
AAG	CAG	GGT	TGC	AAA	ACC	TGT	AGC	TTG	GGA	ACA	TTT	AAT	GAC	CAG	AAC	384	
Lys	Gln	Gly	Cys	Lys	Thr	Cys	Ser	Leu	Gly	Thr	Phe	Asn	Asp	Gln	Asn		
					90				95					100		105	
GGT	ACT	GGC	GTC	TGT	CGA	CCC	TGG	ACG	AAC	TGC	TCT	CTA	GAC	GGA	AGG	432	
Gly	Thr	Gly	Val	Cys	Arg	Pro	Trp	Thr	Asn	Cys	Ser	Leu	Asp	Gly	Arg		
					110				115					120			

TCT GTG CTT AAG ACC GGG ACC ACG GAG AAG GAC GTG GTG TGT GGA CCC Ser Val Leu Lys Thr Gly Thr Glu Lys Asp Val Val Cys Gly Pro 125 130 135	480
CCT GTG GTG AGC TTC TCT CCC AGT ACC ACC ATT TCT GTG ACT CCA GAG Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu 140 145 150	528
GGA GGA CCA GGA GGG CAC TCC TTG CAG GTC CTT ACC TTG TTC CTG GCG Gly Gly Pro Gly Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu Ala 155 160 165	576
CTG ACA TCG GCT TTG CTG CTG GCC CTG ATC TTC ATT ACT CTC CTG TTC Leu Thr Ser Ala Leu Leu Ala Leu Ile Phe Ile Thr Leu Leu Phe 170 175 180 185	624
TCT GTG CTC AAA TGG ATC AGG AAA AAA TTC CCC CAC ATA TTC AAG CAA Ser Val Leu Lys Trp Ile Arg Lys Lys Phe Pro His Ile Phe Lys Gln 190 195 200	672
CCA TTT AAG AAG ACC ACT GGA GCA GCT CAA GAG GAA GAT GCT TGT AGC Pro Phe Lys Lys Thr Thr Gly Ala Ala Gln Glu Glu Asp Ala Cys Ser 205 210 215	720
TGC CGA TGT CCA CAG GAA GAA GGA GGA GGA GGA GGA GGC TAT GAG CTG Cys Arg Cys Pro Gln Glu Glu Gly Gly Gly Gly Tyr Glu Leu 220 225 230	768

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Asn Asn Cys Tyr Asn Val Val Val Ile Val Leu Leu Leu Val -23 -20 -15 -10
Gly Cys Glu Lys Val Gly Ala Val Gln Asn Ser Cys Asp Asn Cys Gln -5 1 5
Pro Gly Thr Phe Cys Arg Lys Tyr Asn Pro Val Cys Lys Ser Cys Pro 10 15 20 25
Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn Cys Asn Ile Cys 30 35 40
Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr 45 50 55
His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro 60 65 70
Gln Cys Thr Arg Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr 75 80 85

Lys	Gln	Gly	Cys	Lys	Thr	Cys	Ser	Leu	Gly	Thr	Phe	Asn	Asp	Gln	Asn
90					95				100					105	
Gly	Thr	Gly	Val	Cys	Arg	Pro	Trp	Thr	Asn	Cys	Ser	Leu	Asp	Gly	Arg
			110					115					120		
Ser	Val	Leu	Lys	Thr	Gly	Thr	Glu	Lys	Asp	Val	Val	Cys	Gly	Pro	
			125				130					135			
Pro	Val	Val	Ser	Phe	Ser	Pro	Ser	Thr	Thr	Ile	Ser	Val	Thr	Pro	Glu
			140			145				150					
Gly	Gly	Pro	Gly	Gly	His	Ser	Leu	Gln	Val	Leu	Thr	Leu	Phe	Leu	Ala
					155		160				165				
Leu	Thr	Ser	Ala	Leu	Leu	Leu	Ala	Leu	Ile	Phe	Ile	Thr	Leu	Leu	Phe
170					175				180			185			
Ser	Val	Leu	Lys	Trp	Ile	Arg	Lys	Lys	Phe	Pro	His	Ile	Phe	Lys	Gln
				190				195			—	200			
Pro	Phe	Lys	Lys	Thr	Thr	Gly	Ala	Ala	Gln	Glu	Glu	Asp	Ala	Cys	Ser
				205				210				215			
Cys	Arg	Cys	Pro	Gln	Gl	Gl	Gl	Gly	Gly	Gly	Gly	Tyr	Glu	Leu	
				220				225				230			

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: hu4-1BB

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 120..887

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 189..884

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 120..188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGTGGAAAGT TCTCCGGCAG CCCTGAGATC TCAAGAGTGA CATTGTGAG ACCAGCTAAT	60
TTGATTAAAA TTCTCTTGGG ATCAGCTTG CTAGTATCAT ACCTGTGCCA GATTCATC	119
ATG GGA AAC AGC TGT TAC AAC ATA GTA GCC ACT CTG TTG CTG GTC CTC Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu	167
-23 -20 -15 -10	
AAC TTT GAG AGG ACA AGA TCA TTG CAG GAT CCT TGT AGT AAC TGC CCA Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro	215
-5 1 5	
GCT GGT ACA TTC TGT GAT AAT AAC AGG AAT CAG ATT TGC AGT CCC TGT Ala Gly Thr Phe Cys Asp Asn Arg Asn Gln Ile Cys Ser Pro Cys	263
10 15 20 25	
CCT CCA AAT AGT TTC TCC AGC GCA GGT GGA CAA AGG ACC TGT GAC ATA Pro Pro Asn Ser Phe Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile	311
30 35 - 40	
TGC AGG CAG TGT AAA GGT GTT TTC AGG ACC AGG AAG GAG TGT TCC TCC Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser	359
45 50 55	
ACC AGC AAT GCA GAG TGT GAC TGC ACT CCA GGG TTT CAC TGC CTG GGG Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly	407
60 65 70	
GCA GGA TGC AGC ATG TGT GAA CAG GAT TGT AAA CAA GGT CAA GAA CTG Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu	455
75 80 85	
ACA AAA AAA GGT TGT AAA GAC TGT TGC TTT GGG ACA TTT AAC GAT CAG Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln	503
90 95 100 105	
AAA CGT GGC ATC TGT CGA CCC TGG ACA AAC TGT TCT TTG GAT GGA AAG Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys	551
110 115 120	
TCT GTG CTT GTG AAT GGG ACG AAG GAG AGG GAC GTG GTC TGT GGA CCA Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro	599
125 130 135	
TCT CCA GCC GAC CTC TCT CCG GGA GCA TCC TCT GTG ACC CCG CCT GCC Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala	647
140 145 150	
CCT GCG AGA GAG CCA GGA CAC TCT CCG CAG ATC ATC TCC TTC TTT CTT Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu	695
155 160 165	
GCG CTG ACG TCG ACT GCG TTG CTC TTC CTG CTG TTC TTC CTC ACG CTC Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu	743
170 175 180 185	

CGT TTC TCT GTT GTT AAA CGG GGC AGA AAG AAA CTC CTG TAT ATA TTC	791
Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe	
190 195 200	
AAA CAA CCA TTT ATG AGA CCA GTA CAA ACT ACT CAA GAG GAA GAT GGC	839
Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly	
205 210 215	
TGT AGC TGC CGA TTT CCA GAA GAA GAA GGA GGA TGT GAA CTG TGAAATGGAA	
894	
Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu	
220 225 230	
GTCAATAGGG CTGTTGGAC TTTCTTGAAA AGAACAGG AAATATGAGT CATCCGCTAT	954
CACAGCTTTC AAAAGCAAGA ACACCACCT ACATAATACC CAGGATTCCC CCAACACACG	1014
TTCTTTCTA AATGCCAATG AGTTGGCCTT TAAAAATGCA CCACCTTTTT TTTTTTTTT	1074
GACAGGGTCT CACTCTGTCA CCCAGGCTGG AGTGCAGTGG CACCACCATG GCTCTCTGCA	1134
GCCTTGACCT CTGGGAGCTC AAGTGATCCT CCTGCCTCAG TCTCCTAGTA GCTGGAACTA	1194
CAAGGAAGGG CCACCACACC TGACTAACTT TTTGTTTTT TGTTGGTAA AGATGGCATT	1254
TCGCCATGTT GTACAGGCTG GTCTCAAAC CCTAGGTTCA CTTTGGCCTC CCAAAGTGCT	1314
GGGATTACAG ACATGAAC TG CCAGGCCGG CCAAAATAAT GCACCACTT TAACAGAAC	1374
GACAGATGAG GACAGAGCTG GTGATAAAAA AAAAAAAAAA A	1415

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu	
-23 -20 -15 -10	
Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro	
-5 1 5	
Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys	
10 15 20 25	
Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile	
30 35 40	
Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser	
45 50 55	
Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly	
60 65 70	

Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu
 75 80 85

Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln
 90 95 100 105

Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys
 110 115 120

Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro
 125 130 135

Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala
 140 145 150

Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu
 155 160 165

Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu
 170 175 180 — 185

Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
 190 195 200

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
 205 210 215

Cys Ser Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu
 220 225 230

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTCACTAGTT CTGTGCAGAA CTCCTGTGAT AAC
 33

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CACAAGATCT GGGCTCCTCT GGAGTCACAG AAATG
35

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CAGACTAGTT CACTCTGGAG TCACAGAAAT G
31

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATAGCGGCCG CTGCCAGATT TCATCATGGG AAAC
34

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACAAGATCTG GGCTCCTGCG GAGAGTGTCC TGGCTCTCTC
40

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: hIgG1Fc

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

G	GTA	CCG	CTA	GCG	TCG	ACA	GGC	CTA	GGA	TAT	CGA	TAC	GTA	GAG	CCC	46
Val	Pro	Leu	Ala	Ser	Thr	Gly	Leu	Gly	Tyr	Arg	Tyr	Val	Glu	Pro		
1									10					15		
AGA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA	GCA	CCT	GAA	94
Arg	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	
									25					30		
CTC	CTG	GGG	GGA	CCG	TCA	GTC	TTC	CTC	TTC	CCC	CCA	AAA	CCC	AAG	GAC	142
Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	
									40					45		
ACC	CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACA	TGC	GTG	GTG	GTG	GAC	190
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	
									50					60		
GTG	AGC	CAC	GAA	GAC	CCT	GAG	GTC	AAG	TTC	AAC	TGG	TAC	GTG	GAC	GGC	238
Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	
								65						75		
GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	AAG	CCG	CGG	GAG	GAG	CAG	TAC	AAC	286
Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	
								80						95		
AGC	ACG	TAC	CGG	GTG	GTC	AGC	GTC	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	334
Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	
								100						110		
CTG	AAT	GGC	AAG	GAC	TAC	AAG	TGC	AAG	GTC	TCC	AAC	AAA	GCC	CTC	CCA	382
Leu	Asn	Gly	Lys	Asp	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	
								115						125		
GCC	CCC	ATG	CAG	AAA	ACC	ATC	TCC	AAA	GCC	AAA	GGG	CAG	CCC	CGA	GAA	430
Ala	Pro	Met	Gln	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	
								130						140		

CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC	478
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn	
145 150 155	
CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGG CAC ATC	526
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg His Ile	
160 165 170 175	
GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC	574
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr	
180 185 190	
ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG	622
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys	
195 200 205	
CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC	670
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys	
210 215 220	
TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC	718
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu	
225 230 235	
TCC CTG TCT CCG GGT AAA TGAACCTAGT	745
Ser Leu Ser Pro Gly Lys	
240 245	

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Val Pro Leu Ala Ser Thr Gly Leu Gly Tyr Arg Tyr Val Glu Pro Arg	
1 5 10 15	
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu	
20 25 30	
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr	
35 40 45	
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val	
50 55 60	
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val	
65 70 75 80	
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser	
85 90 95	

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
100 105 110

Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
115 120 125

Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
130 135 140

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
145 150 155 160

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg His Ile Ala
165 170 175

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
180 185 190

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
195 200 205

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
210 215 220

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
225 230 235 240

Leu Ser Pro Gly Lys
245